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RAW SEQUENCE LISTING DATE: 08/07/2002
PATENT APPLICATION: **US/09/892,613C** TIME: 09:37:23

Input Set : **A:\09892613.ST25.txt**
Output Set: **N:\CRF3\08072002\I892613C.raw**

```
      3 <110> APPLICANT: Leung, Shawn Shui-on
      5 <120> TITLE OF INVENTION: REDUCING IMMUNOGENICITIES OF IMMUNOGLOBULINS BY FRAMEWORK-
PATCHING
      7 <130> FILE REFERENCE: 655
      9 <140> CURRENT APPLICATION NUMBER: US 09/892,613C
     10 <141> CURRENT FILING DATE: 2001-06-27
     12 <160> NUMBER OF SEQ ID NOS: 32
     14 <170> SOFTWARE: PatentIn version 3.1
     16 <210> SEQ ID NO: 1
     17 <211> LENGTH: 369
     18 <212> TYPE: DNA
     19 <213> ORGANISM: Artificial Sequence
     21 <220> FEATURE:
     22 <223> OTHER INFORMATION: FR-patched heavy chaim variable region sequence (Full DNA
Sequenc
     23       e) formed by joining the N- and C- terminal (SEQ 3 and 6) halves
     24       at the KpeI site.
     26 <220> FEATURE:
     27 <221> NAME/KEY: V_region
     28 <222> LOCATION: (1)..(369)
     29 <223> OTHER INFORMATION:
     32 <400> SEQUENCE: 1
     33 gaagtgcagc tgctggagtc tgggggaggc ttagtgcagc ctggagggtc cctgaggctc     60
     35 tcctgtgcag cctctggatt ctccttcagt atctatgaca tgtcttgggt tcgccaggca    120
     37 ccgggaaagg ggctggagtg ggtcgcatac attagtagtg gtggtggtac cacctactat    180
     39 ccagacactg tgaagggccg attcaccatc tccagagaca atgccaagaa ctccctgtac    240
     41 ctgcaaatga acagtctgag ggtggaggac acagccttat attactgtgc aagacatagt    300
     43 ggctacggta gtagctacgg ggttttgttt gcttactggg gccaagggac tctggtcact    360
     45 gtctcttca                                                           369
     48 <210> SEQ ID NO: 2
     49 <211> LENGTH: 123
     50 <212> TYPE: PRT
     51 <213> ORGANISM: Chimaera sp.
     53 <400> SEQUENCE: 2
     55 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
     56 1               5                  10                  15
     59 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ile Tyr
     60             20                  25                  30
     63 Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
     64         35                  40                  45
     67 Ala Tyr Ile Ser Ser Gly Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Val
     68     50                  55                  60
     71 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
     72 65                  70                  75                  80
```

75 Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Leu Tyr Tyr Cys

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```
     76                 85                  90                  95
     79 Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr
     80             100                 105                 110
     83 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
     84         115                 120
     87 <210> SEQ ID NO: 3
     88 <211> LENGTH: 111
     89 <212> TYPE: DNA
     90 <213> ORGANISM: Artificial Sequence
     92 <220> FEATURE:
     93 <223> OTHER INFORMATION: N-template is a synthetic sense-strand oligonucleotide
encoding a
     94       mino acide 14-50 of the VH region (SEQ ID No. 2). The template is
     95       PCR-amplified by two primers (SEQ ID No. 4 and 5)
     97 <220> FEATURE:
     98 <221> NAME/KEY: V_region
     99 <222> LOCATION: (1)..(111)
    100 <223> OTHER INFORMATION:
    103 <400> SEQUENCE: 3
    104 cctggagggt ccctgaggct ctcctgtgca gcctctggat tctccttcag tatctatgac     60
    106 atgtcttggg ttcgccaggc accgggaaag gggctggagt gggtcgcata c             111
    109 <210> SEQ ID NO: 4
    110 <211> LENGTH: 57
    111 <212> TYPE: DNA
    112 <213> ORGANISM: Artificial Sequence
    114 <220> FEATURE:
    115 <223> OTHER INFORMATION: 5' Primer is a synthetic sense-strand oligonucleotide
encoding am
    116       ino acid 1-19 of the VH region (SEQ ID No. 2). The 3' end of the
    117       primer overlaps with the 5'end of the template by 18 nucleotides
    118       .
    120 <220> FEATURE:
    121 <221> NAME/KEY: primer_bind
    122 <222> LOCATION: (1)..(57)
    123 <223> OTHER INFORMATION:
    126 <400> SEQUENCE: 4
    127 gaagtgcagc tgctggagtc tgggggaggc ttagtgcagc ctggagggtc cctgagg        57
    130 <210> SEQ ID NO: 5
    131 <211> LENGTH: 48
    132 <212> TYPE: DNA
    133 <213> ORGANISM: Artificial Sequence
    135 <220> FEATURE:
    136 <223> OTHER INFORMATION: 3' Primer is a synthetic anti-sense-strand oligonucleotide
encodi
    137       ng amino acid 43-59 of the VH region(SEQ ID No. 2). The primer o
    138       verlaps with the template by 21 nucleotides.
    140 <220> FEATURE:
    141 <221> NAME/KEY: primer_bind
    142 <222> LOCATION: (1)..(48)
    143 <223> OTHER INFORMATION:
    146 <400> SEQUENCE: 5
    147 gtaggtggta ccaccaccac tactaatgta tgcgacccac tccagccc                  48
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     150 <210> SEQ ID NO: 6
     151 <211> LENGTH: 132
     152 <212> TYPE: DNA
     153 <213> ORGANISM: Artificial Sequence
     155 <220> FEATURE:
     156 <223> OTHER INFORMATION: C-terminal is a synthetic sense-strand oligonucleotide
encoding a
     157       mino acid 68-111 of the VH region (SEQ ID No 2) The template is P
     158       CR-amplified by two primers (SEQ ID No 7 and 8)
     160 <220> FEATURE:
     161 <221> NAME/KEY: V_region
     162 <222> LOCATION: (1)..(132)
     163 <223> OTHER INFORMATION:
     166 <400> SEQUENCE: 6
     167 ttcaccatct ccagagacaa tgccaagaac tccctgtacc tgcaaatgaa cagtctgagg     60
     169 gtggaggaca cagccttata ttactgtgca agacatagtg gctacggtag tagctacggg    120
     171 gttttgtttg ct                                                      132
     174 <210> SEQ ID NO: 7
     175 <211> LENGTH: 60
     176 <212> TYPE: DNA
     177 <213> ORGANISM: Artificial Sequence
     179 <220> FEATURE:
     180 <223> OTHER INFORMATION: 5' Primer is a synthetic sense-strand oligonucleotide
encoding am
     181       ino acid 55-74 of the VH region (SEQ ID No 2). The 3' end of the
     182       primer overlaps with the 5'end of the template by 21 nucleotides
     183       .
     185 <220> FEATURE:
     186 <221> NAME/KEY: primer_bind
     187 <222> LOCATION: (1)..(60)
     188 <223> OTHER INFORMATION:
     191 <400> SEQUENCE: 7
     192 ggtggtacca cctactatcc agacactgtg aagggccgat tcaccatctc cagagacaat     60
     195 <210> SEQ ID NO: 8
     196 <211> LENGTH: 57
     197 <212> TYPE: DNA
     198 <213> ORGANISM: Artificial Sequence
     200 <220> FEATURE:
     201 <223> OTHER INFORMATION: 3' Primer is a synthetic anti-sense-strand oligonucleotide
encodi
     202       ng amino acid 105-123 of the VH region (SEQ ID No 2). The primer
     203       and the template overlaps by 21 nucleotides.
     205 <220> FEATURE:
     206 <221> NAME/KEY: primer_bind
     207 <222> LOCATION: (1)..(57)
     208 <223> OTHER INFORMATION:
     211 <400> SEQUENCE: 8
     212 tgaagagaca gtgaccagag tcccttggcc ccagtaagca aacaaaaccc cgtagct        57
     215 <210> SEQ ID NO: 9
     216 <211> LENGTH: 321
     217 <212> TYPE: DNA
     218 <213> ORGANISM: Artificial Sequence
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220 <220> FEATURE:
221 <223> OTHER INFORMATION: FR-patched light chaim variable region sequence formed by joining
222 the N- and C- terminal (SEQ 11 and 14) halves at the KpeI site.
224 <220> FEATURE:
225 <221> NAME/KEY: V_region
226 <222> LOCATION: (1)..(321)
227 <223> OTHER INFORMATION:
230 <400> SEQUENCE: 9
231 gatatccaga tgacccagtc tccatcctcc ctgtctgcct ctgtgggaga cagagtcacc 60
233 attagttgca gggcaagtca ggacattagc aattatttaa actggtatca gcagaaacca 120
235 ggtaaggctc cgaaactcct gatctactac actagtatat tacactcagg agtcccatca 180
237 aggttcagtg gcagtgggtc tggaacagaa tttactctca ccattagctc cctgcagcca 240
239 gaagattttg ccacttactt ttgccaacag ggtaatacgc ttccgtggac gttcggtgga 300
241 ggcaccaagg tggaaatcaa a 321
244 <210> SEQ ID NO: 10
245 <211> LENGTH: 107
246 <212> TYPE: PRT
247 <213> ORGANISM: Chimaera sp.
249 <400> SEQUENCE: 10
251 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
252 1 5 10 15
255 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
256 20 25 30
259 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
260 35 40 45
263 Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
264 50 55 60
267 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
268 65 70 75 80
271 Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
272 85 90 95
275 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
276 100 105
279 <210> SEQ ID NO: 11
280 <211> LENGTH: 108
281 <212> TYPE: DNA
282 <213> ORGANISM: Artificial Sequence
284 <220> FEATURE:
285 <223> OTHER INFORMATION: N-template is a synthetic sense-strand oligonucleotide encoding a
286 mino acid 11-46 of the VL region (SEQ ID No. 10). The template is
287 PCR-amplified by two primers (SEQ ID No. 12 and 13)
289 <220> FEATURE:
290 <221> NAME/KEY: V_region
291 <222> LOCATION: (1)..(108)
292 <223> OTHER INFORMATION:
295 <400> SEQUENCE: 11
296 ctgtctgcct ctgtgggaga cagagtcacc attagttgca gggcaagtca ggacattagc 60
298 aattatttaa actggtatca gcagaaacca ggtaaggctc cgaaactc 108
301 <210> SEQ ID NO: 12

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Input Set : A:\09892613.ST25.txt
Output Set: N:\CRF3\08072002\I892613C.raw

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     302 <211> LENGTH: 51
     303 <212> TYPE: DNA
     304 <213> ORGANISM: Artificial Sequence
     306 <220> FEATURE:
     307 <223> OTHER INFORMATION: 5' Primer is a synthetic sense-strand oligonucleotide
encoding am
     308       ino acid 1-17 of the VH region (SEQ ID No 10). The 3' end of the
     309       primer overlaps with the 5'end of the template by 21 nucleotides
     310       .
     312 <220> FEATURE:
     313 <221> NAME/KEY: primer_bind
     314 <222> LOCATION: (1)..(51)
     315 <223> OTHER INFORMATION:
     318 <400> SEQUENCE: 12
     319 gatatccaga tgacccagtc tccatcctcc ctgtctgcct ctgtgggaga c              51
     322 <210> SEQ ID NO: 13
     323 <211> LENGTH: 40
     324 <212> TYPE: DNA
     325 <213> ORGANISM: Artificial Sequence
     327 <220> FEATURE:
     328 <223> OTHER INFORMATION: 3' Primer is a synthetic anti-sense-strand oligonucleotide
encodi
     329       ng amino acid 40-53. The primer and the template overlaps by 18
     330       nucleotides.
     332 <220> FEATURE:
     333 <221> NAME/KEY: primer_bind
     334 <222> LOCATION: (1)..(40)
     335 <223> OTHER INFORMATION:
     338 <400> SEQUENCE: 13
     339 atatactagt gtagtagatc aggagtttcg gagccttacc                          40
     342 <210> SEQ ID NO: 14
     343 <211> LENGTH: 120
     344 <212> TYPE: DNA
     345 <213> ORGANISM: Artificial Sequence
     347 <220> FEATURE:
     348 <223> OTHER INFORMATION: C-terminal is a synthetic sense-strand oligonucleotide
encoding a
     349       mino acid 59-98 of the VH region (SEQ ID No 10) The template is P
     350       CR-amplified by tow primers (SEQ ID No 15 and 16)
     352 <220> FEATURE:
     353 <221> NAME/KEY: V_region
     354 <222> LOCATION: (1)..(120)
     355 <223> OTHER INFORMATION:
     358 <400> SEQUENCE: 14
     359 ccatcaaggt tcagtggcag tgggtctgga acagaattta ctctcaccat tagctccctg     60
     361 cagccagaag attttgccac ttacttttgc caacagggta atacgcttcc gtggacgttc    120
     364 <210> SEQ ID NO: 15
     365 <211> LENGTH: 49
     366 <212> TYPE: DNA
     367 <213> ORGANISM: Artificial Sequence
     369 <220> FEATURE:
     370 <223> OTHER INFORMATION: 5' Primer is a synthetic sense-strand oligonucleotide
encoding am
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VERIFICATION SUMMARY DATE: 08/07/2002
PATENT APPLICATION: **US/09/892,613C** TIME: 09:37:24

Input Set : **A:\09892613.ST25.txt**
Output Set: **N:\CRF3\08072002\I892613C.raw**